

Fig. 2

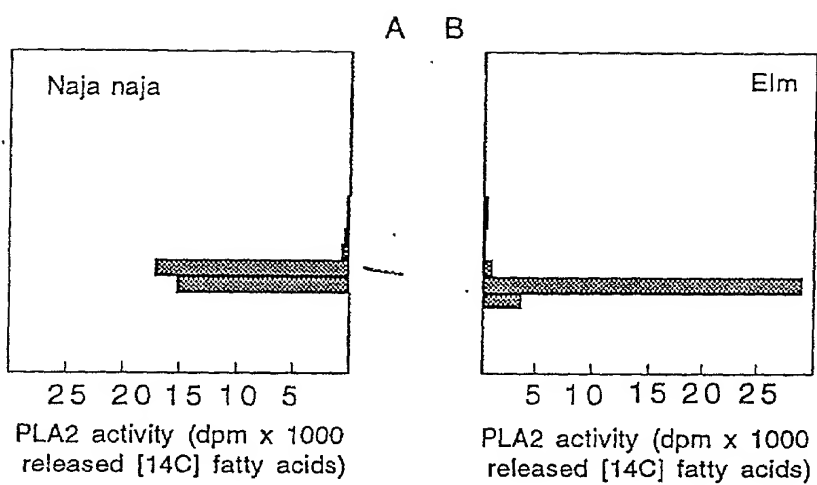


Fig. 3

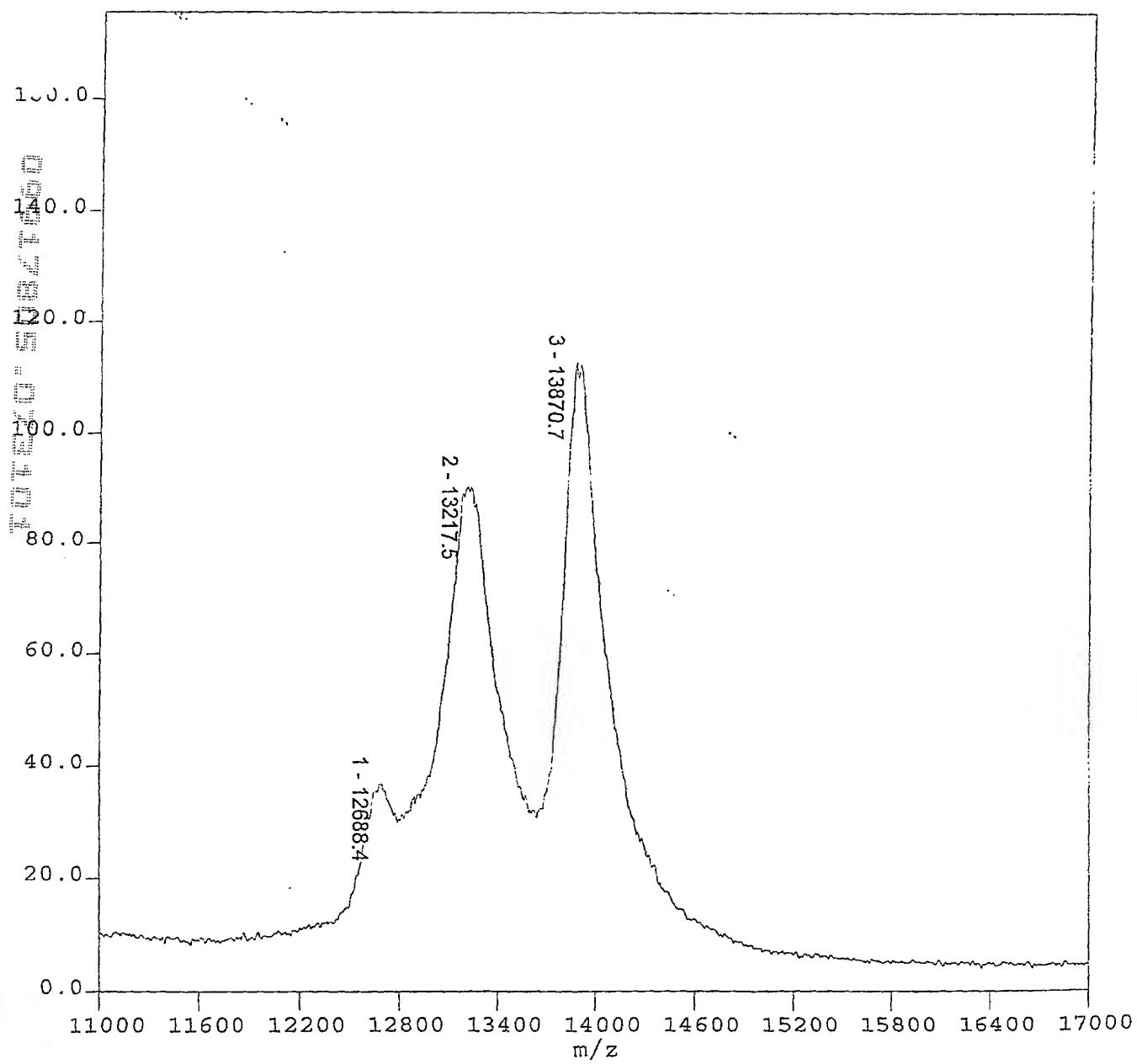


Fig. 4

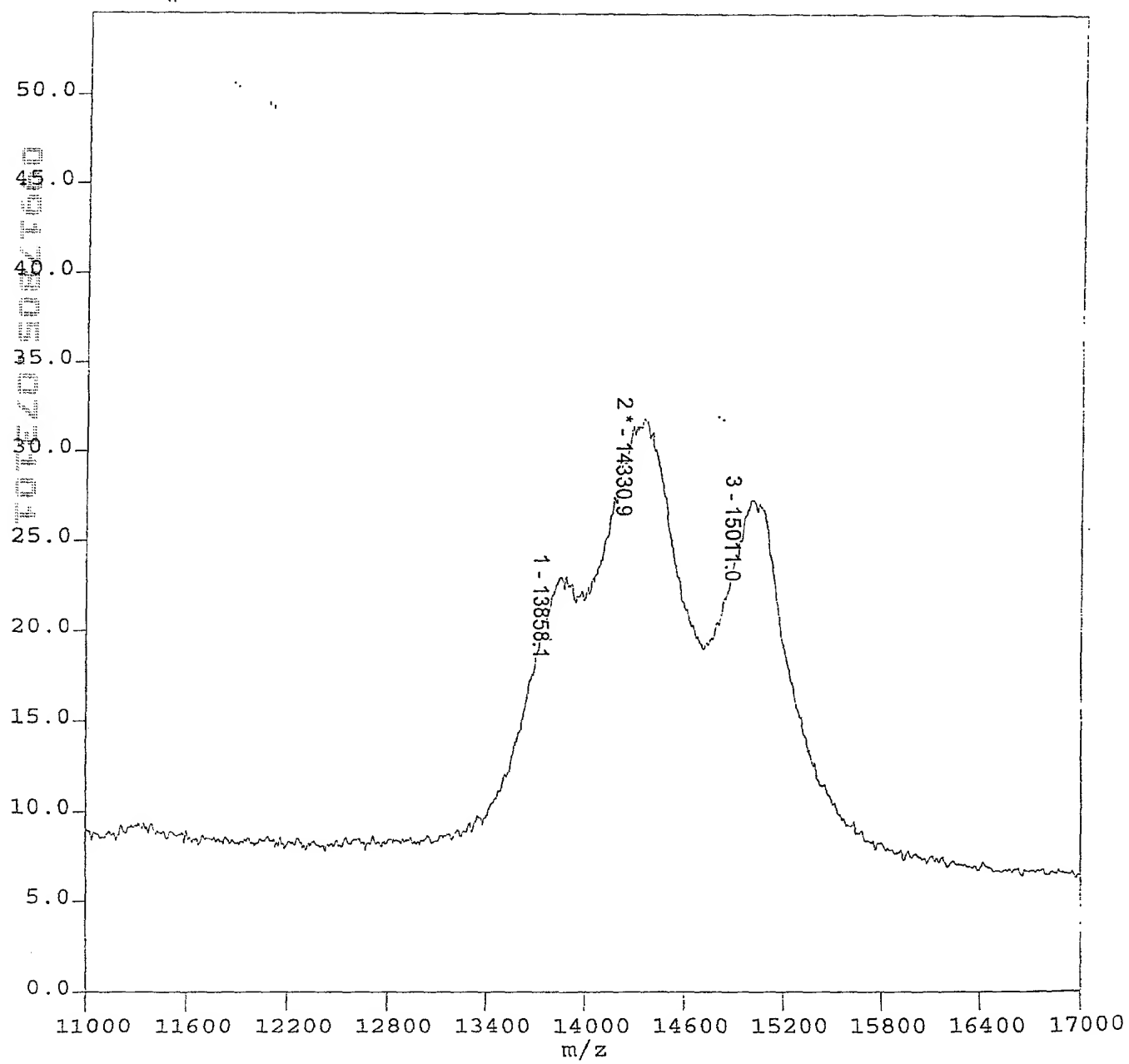


Fig. 5.

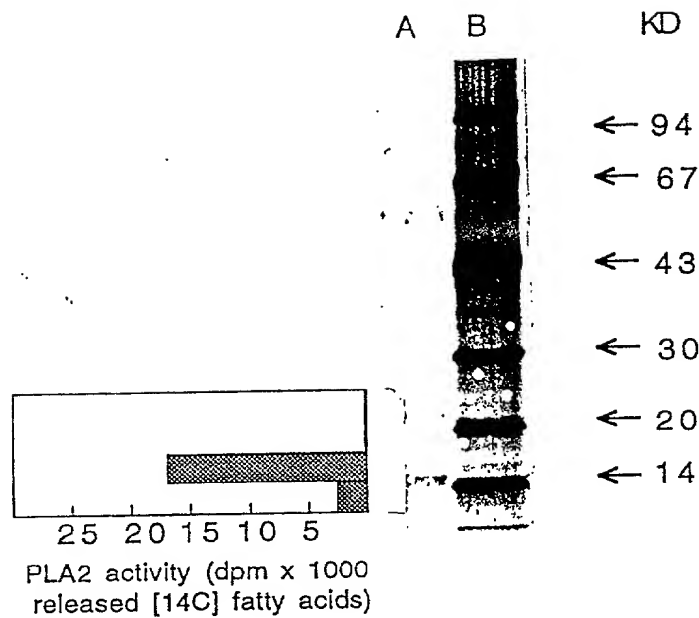


Fig. 6

D49050	MP--PRSHLL	A--LVFLA-A	GVLSA--TS	PPPPPCSRSC	AALNCDSVGI	43
D00035	MKFLVLAALL	T--VAAAE-G	GISPRA--VW	QFRNMIKC-TI	PESDPLKDYN	45
D10070	MR-----TLW	I--MAVLL-V	GV-DGG--LW	QFENMIKV	KKSGILES-YS	38
M21054	MKLLVLAALL	T--VAAAD-S	GISPRA--VW	QFRMIKCVI	PGSDPFLEYN	45
X12605	MPAHLVLL	TVCVSLLEAS	SIPARPLNLY	QFGNMIQCAN	HGRRPTLAYA	50
X53406	MNPAHLVLL	AVCVSLLGAA	NVPPQHLNLY	QFKNMIVC--	AGTRPWIGYV	48
X53471	MR-----TLW	I--VAVCL-I	GV-EGS--LL	EFGMMILGE-	TGKNPLTSYS	38
X76289	MR-----TLW	I--MAVLL-V	GV-EGD--LW	QFGQMILKE-	TGKLPPPYT	38
Y00120	MRLVLAALL	T--VGAGQ-A	GLNSRA--LW	QFNGMIKCKI	PSSEPLLDNF	45
Y00377	MPAHLVLL	AVCVSLLGAS	AIPPLPLNLA	QFALVIKCAD	KGRRPRWHYM	50

D49050	RYGKYCGMGW	SGCDGEEPCD	DLDCCKTHD	HC-VDKKGLM	SVKC--HEKF	90
D00035	DYGYCGLG	SG---TPMD	ELDCCKTHD	HCYSEAKKLD	SCKFLLDNPNY	91
D10070	RYGYCGMG	RG---KPKD	ATDCCKVHD	CCYGVKVTGCN	P-KL-GKTY	82
M21054	NYGYCGLG	SG---TPMD	ELDCCKTHD	NCYDQAKKLD	SCKFLLDNPNY	91
X12605	DYGYCGAGG	SG---TPMD	ELDCCKVHD	DCYGEAGK-K	GC-Y---PTL	91
X53406	NYGYCGAGG	SG---TPMD	ELDCCKVHD	NCYGEAEKIP	GC-----NPK	89
X53471	FYGYCGAGG	KG---TPMD	ATDCCKVHD	CCYGN---LP	DC-----SPK	76
X76289	TYGYCGAGG	QG---QPKD	ATDCCKVHD	CCYG---KLT	NC-----KPK	76
Y00120	NYGYCGLG	SG---TPMD	DLDCCKTHD	NCYKQAKKLD	SCKVLVDNPNY	91
Y00377	DYGYCGFGG	SG---TPMD	ELDCCKTHD	CCYQAQAEK-K	GC-----YPK	90

Fig. 6 cont.

D49050	KNCMRKVKKA	GKIGFSRK--	CPYEMAMAT	MTSGMDMAIM	-----LS-Q	130
D00035	TKIYSYSCSG	SEITCSSKNK	DCQAFICNCD	RSAAICFSKA	-----PY-N	134
D10070	SWNNGDIVCE	GDGPKCEVC-	ECDRAAAI CF	RDNLDTYDRN	-----KYWR	125
M21054	THIYSYSCSG	SAITCSSKNK	ECFAFICNCD	RNAAICFSKA	-----PY-N	134
X12605	T-LYSWQIE	KTPTCNSKT-	GCERSVDCD	ATAAKCFKA	-----PY-N	132
X53406	TKTYSYTCTK	PNLTCTDAAG	TCARRIVDCD	RTAAICFAAA	-----PY-N	132
X53471	TDRYKYHREN	GAIVCGKGT-	SCENRICECD	RAAAICFRKN	LKTYNYIYRN	125
X76289	TDRYSYSREN	GVIICGEGT-	FCEKQICECD	KAAAVCFREN	LRTYKKRYMA	125
Y00120	TNNYSYSCSN	NEITCSSENN	ACEAFICNCD	RNAAICFSKV	-----PY-N	134
Y00377	LTMYSYCGG	DGPYCNSKT-	ECQRFVDCD	VRAADCFARY	-----PY-N	132

D49050	LGTKLEL
D00035	KEHKNLDTKKYC
D10070	YPASNCQEDSEPC
M21054	KAHKNLDTKKYCQS
X12605	KKNYNIDTEKRCQ
X53406	TNNFMISSTHCQ
X53471	YPDFLCKKESEKC
X76289	YPDVLCKKPAEKC
Y00120	KEHKNLDTKKYC
Y00377	NKNYNINTSKRCK

1	16	31
N-terminal-----	-----XN/GVQ	ATGTSISVGKCCXPK
D47724	MRFFLKLAAPRCVLLL	LLGVTPAKDQCCSRIT
D47653	MRFFLKLAAPRCVLLL	LLGVTPAKDQCCSRIT
D49050	-----MPPRSPLIAL	SATSPPPP--CPRS

Fig. 7

46	61	76	30	83	88	76
CXXXFCYGP	KYCGILYSGCPGERP	CDALDXCC				
CESQFCTIAPLLRYG	KYCGILYSGCPGERP	CDGXDXCMVHDH				
CESQFCTIAPLLRYG	KYCGVGVSGCDGEFP	CDDLDAACCRDHDHCV				
CAALNCDSVG-IRYG						

Ca²⁺-binding site active site